```
BLASTP 2.2.20+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.


RID: YSX8TCPP011



Database: Non-redundant SwissProt sequences
           383,955 sequences; 142,559,671 total letters

Query=
Length=16
```

No significant similarity found. For reasons why, <u>click here</u>.

```
  Database: Non-redundant SwissProt sequences
    Posted date:  Apr 17, 2009  6:11 PM
  Number of letters in database: 43,926
  Number of sequences in database:  583

Lambda      K        H
   0.335    0.297     1.50
Gapped
Lambda      K        H
   0.294    0.110     0.610
Matrix: PAM30
Gap Penalties: Existence: 9, Extension: 1
Number of Sequences: 583
Number of Hits to DB: 4781
Number of extensions: 261
Number of successful extensions: 261
Number of sequences better than 200000: 161
Number of HSP's better than 200000 without gapping: 0
Number of HSP's gapped: 228
Number of HSP's successfully gapped: 214
Length of query: 16
Length of database: 43926
Length adjustment: 6
Effective length of query: 10
Effective length of database: 40428
Effective search space: 404280
Effective search space used: 404280
T: 11
A: 40
X1: 1 (0.5 bits)
X2: 35 (14.8 bits)
X3: 58 (24.6 bits)
S1: 1 (3.6 bits)
S2: 0 (3.2 bits)
```